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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/847,046

DATE: 09/27/2001

TIME: 14:59:44

Input Set : A:\ES.txt

Output Set: N:\CRF3\09272001\I847046.raw

ENTERED

3 <110> APPLICANT: Hevezi, Peter
 4 Mack, David
 5 Gish, Kurt C.
 6 Wilson, Keith E.
 8 <120> TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF PROSTATE AND/OR BREAST CANCER,
 9 COMPOSITIONS, AND METHODS OF SCREENING FOR PROSTATE CANCER AND/OR BREAST CANCER
 10 MODULATORS
 12 <130> FILE REFERENCE: A-69199-1/DJB/JJD/AMS
 14 <140> CURRENT APPLICATION NUMBER: US 09/847,046
 15 <141> CURRENT FILING DATE: 2001-04-30
 17 <150> PRIOR APPLICATION NUMBER: US 09/733,288
 18 <151> PRIOR FILING DATE: 2000-12-08
 20 <150> PRIOR APPLICATION NUMBER: US 09/687,576
 21 <151> PRIOR FILING DATE: 2000-10-13
 23 <160> NUMBER OF SEQ ID NOS: 3
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 4526
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
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 55 tccctactga caccctgttt gatgtgaatg ccattgtcgc ccatgttctc tttgtctctc 720
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91	agaacccagt	atccttatgct	ggaatgttag	gaaccaaaga	tctcctaaaa	tttatccagc	1800
93	tcaacaggat	ttcatatcca	gtgaatataa	catcgatoca	agaagcagaa	gaatatttta	1860
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183 agaatacctt caaaaaaaaa aaaaaa
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 807
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 2
193 Met Phe Ser Gly Phe Asn Val Phe Arg Val Gly Ile Ser Phe Val Ile
194 1 5 10 15
197 Met Cys Ile Phe Tyr Met Pro Thr Val Asn Ser Leu Pro Glu Leu Ser
198 20 25 30
201 Pro Gln Lys Tyr Phe Ser Thr Leu Gln Pro Gly Leu Glu Glu Leu Asn
202 35 40 45
205 Glu Ala Val Arg Pro Leu Gln Asp Tyr Gly Ile Ser Val Ala Lys Val
206 50 55 60
209 Asn Cys Val Lys Glu Glu Ile Ser Arg Tyr Cys Gly Lys Glu Lys Asp
210 65 70 75 80
213 Leu Met Lys Ala Tyr Leu Phe Lys Gly Asn Ile Leu Leu Arg Glu Phe
214 85 90 95
217 Pro Thr Asp Thr Leu Phe Asp Val Asn Ala Ile Val Ala His Val Leu
218 100 105 110
221 Phe Ala Leu Leu Phe Ser Glu Val Lys Tyr Ile Thr Asn Leu Glu Asp
222 115 120 125
225 Leu Gln Asn Ile Glu Asn Ala Leu Lys Gly Lys Ala Asn Ile Ile Phe
226 130 135 140
229 Ser Tyr Val Arg Ala Ile Gly Ile Pro Glu His Arg Ala Val Met Glu
230 145 150 155 160
233 Ala Gly Phe Val Tyr Gly Thr Thr Tyr Gln Phe Val Leu Thr Thr Glu
234 165 170 175
237 Ile Ala Leu Leu Glu Ser Ile Gly Ser Glu Asp Val Glu Tyr Ala His
238 180 185 190
241 Leu Tyr Phe Phe His Cys Lys Leu Val Leu Asp Leu Thr Gln Gln Cys
242 195 200 205
245 Arg Arg Thr Leu Met Glu Gln Pro Leu Thr Thr Leu Asn Ile His Leu
246 210 215 220
249 Phe Ile Lys Thr Met Lys Ala Pro Leu Leu Thr Glu Val Ala Glu Asp
250 225 230 235 240
253 Pro Gln Gln Val Ser Thr Val His Leu Gln Leu Gly Leu Pro Leu Val
254 245 250 255
257 Phe Ile Val Ser Gln Gln Ala Thr Tyr Glu Ala Asp Arg Arg Thr Ala
258 260 265 270
261 Glu Trp Val Ala Trp Arg Leu Leu Gly Lys Ala Gly Val Leu Leu Leu
262 275 280 285
265 Leu Arg Asp Ser Leu Glu Val Asn Ile Pro Gln Asp Ala Asn Val Val
266 290 295 300
269 Phe Lys Arg Ala Glu Glu Gly Val Pro Val Glu Phe Leu Val Leu His
270 305 310 315 320
273 Asp Val Asp Leu Ile Ile Ser His Val Glu Asn Asn Met His Ile Glu
274 325 330 335
277 Glu Ile Gln Glu Asp Glu Asp Asn Asp Met Glu Gly Pro Asp Ile Asp

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278          340          345          350
281 Val Gln Asp Asp Glu Val Ala Glu Thr Val Phe Arg Asp Arg Lys Arg
282          355          360          365
285 Lys Leu Pro Leu Glu Leu Thr Val Glu Leu Thr Glu Glu Thr Phe Asn
286          370          375          380
289 Ala Thr Val Met Ala Ser Asp Ser Ile Val Leu Phe Tyr Ala Gly Trp
290 385          390          395          400
293 Gln Ala Val Ser Met Ala Phe Leu Gln Ser Tyr Ile Asp Val Ala Val
294          405          410          415
297 Lys Leu Lys Gly Thr Ser Thr Met Leu Leu Thr Arg Ile Asn Cys Ala
298          420          425          430
301 Asp Trp Ser Asp Val Cys Thr Lys Gln Asn Val Thr Glu Phe Pro Ile
302          435          440          445
305 Ile Lys Met Tyr Lys Lys Gly Glu Asn Pro Val Ser Tyr Ala Gly Met
306          450          455          460
309 Leu Gly Thr Lys Asp Leu Leu Lys Phe Ile Gln Leu Asn Arg Ile Ser
310 465          470          475          480
313 Tyr Pro Val Asn Ile Thr Ser Ile Gln Glu Ala Glu Glu Tyr Leu Ser
314          485          490          495
317 Gly Glu Leu Tyr Lys Asp Leu Ile Leu Tyr Ser Ser Val Ser Val Leu
318          500          505          510
321 Gly Leu Phe Ser Pro Thr Met Lys Thr Ala Lys Glu Asp Phe Ser Glu
322          515          520          525
325 Ala Gly Asn Tyr Leu Lys Gly Tyr Val Ile Thr Gly Ile Tyr Ser Glu
326          530          535          540
329 Glu Asp Val Leu Leu Leu Ser Thr Lys Tyr Ala Ala Ser Leu Pro Ala
330 545          550          555          560
333 Leu Leu Leu Ala Arg His Thr Glu Gly Lys Ile Glu Ser Ile Pro Leu
334          565          570          575
337 Ala Ser Thr His Ala Gln Asp Ile Val Gln Ile Ile Thr Asp Ala Leu
338          580          585          590
341 Leu Glu Met Phe Pro Glu Ile Thr Val Glu Asn Leu Pro Ser Tyr Phe
342          595          600          605
345 Arg Leu Gln Lys Pro Leu Leu Ile Leu Phe Ser Asp Gly Thr Val Asn
346          610          615          620
349 Pro Gln Tyr Lys Lys Ala Ile Leu Thr Leu Val Lys Gln Lys Tyr Leu
350 625          630          635          640
353 Asp Ser Phe Thr Pro Cys Trp Leu Asn Leu Lys Asn Thr Pro Val Gly
354          645          650          655
357 Arg Gly Ile Leu Arg Ala Tyr Phe Asp Pro Leu Pro Pro Leu Pro Leu
358          660          665          670
361 Leu Val Leu Val Asn Leu His Ser Gly Gly Gln Val Phe Ala Phe Pro
362          675          680          685
365 Ser Asp Gln Ala Ile Ile Glu Glu Asn Leu Val Leu Trp Leu Lys Lys
366          690          695          700
369 Leu Glu Ala Gly Leu Glu Asn His Ile Thr Ile Leu Pro Ala Gln Glu
370 705          710          715          720
373 Trp Lys Pro Pro Leu Pro Ala Tyr Asp Phe Leu Ser Met Ile Asp Ala
374          725          730          735

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377 Ala Thr Ser Gln Arg Gly Thr Arg Lys Val Pro Lys Cys Met Lys Glu
378      740      745      750
381 Thr Asp Val Gln Glu Asn Asp Lys Glu Gln His Glu Asp Lys Ser Ala
382      755      760      765
385 Val Arg Lys Glu Pro Ile Glu Thr Leu Arg Ile Lys His Trp Asn Arg
386      770      775      780
389 Ser Asn Trp Phe Lys Glu Ala Glu Lys Ser Phe Arg Arg Asp Lys Glu
390 785      790      795      800
393 Leu Gly Cys Ser Lys Val Asn
394      805

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397 <210> SEQ ID NO: 3

398 <211> LENGTH: 5

399 <212> TYPE: PRT

400 <213> ORGANISM: Unknown

402 <220> FEATURE:

403 <223> OTHER INFORMATION: cytokine receptor extracellular motif found in many species *one*

405 <220> FEATURE:

406 <221> NAME/KEY: MISC_FEATURE

407 <222> LOCATION: (3)..(3)

408 <223> OTHER INFORMATION: "Xaa" at position 3 can be any amino acid.

411 <400> SEQUENCE: 3

W--> 413 Trp Ser Xaa Trp Ser

414 1 5

VERIFICATION SUMMARY

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Input Set : A:\ES.txt

Output Set: N:\CRF3\09272001\I847046.raw

L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3